CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to the nucleotide sequence of either of SEQ ID NOs: 1 and 3;

b) a nucleic acid molecule comprising a fragment of at least 300 nucleotides of the nucleotide sequence of either of SEQ ID NOs: 1 and 3;

c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO: 2;

d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO: 2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO: 2; and

e) a nucleic acid molecule which encodes a naturally-occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO: 2, wherein the nucleic acid molecule hybridizes with a nucleic acid molecule comprising one of SEQ ID NO: 1, SEQ ID NO: 3, and a complement thereof, under stringent conditions.

2. The isolated nucleic acid molecule of claim 1, which is selected from the group consisting of:

a) a nucleic acid comprising the nucleotide sequence of either of SEQ ID NOs: 1 and 3; and

b) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO: 2.

3. The nucleic acid molecule of claim 1 further comprising a vector nucleic acid sequence.

4. The nucleic acid molecule of claim 1 further comprising a nucleic acid sequence encoding a heterologous polypeptide.

5. A host cell that contains the nucleic acid molecule of claim 1.

6. The host cell of claim 5, wherein the host cell is a mammalian host cell.

7. A non-human mammalian host cell containing the nucleic acid molecule of claim 1.

8. An isolated polypeptide selected from the group consisting of:

a) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to a nucleic acid comprising the nucleotide sequence of either of SEQ ID NOs: 1 and 3, and a complement of one of these;

b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO: 2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes with a nucleic acid molecule comprising one of SEQ ID NO: 1, SEQ ID NO: 3, and a complement of either of these under stringent conditions; and

c) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO: 2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO: 2.

9. The isolated polypeptide of claim 8 comprising the amino acid sequence of SEQ ID NO: 2.

10. The polypeptide of claim 8, further comprising a heterologous amino acid sequence.

11. An antibody that selectively binds with a polypeptide of claim 8.

12. A method for producing a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO: 2;

b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO: 2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO: 2; and

c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO: 2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes with a nucleic acid molecule comprising one of SEQ ID NO: 1, SEQ ID NO: 3, and a complement of either of these, under stringent conditions;

the method comprising culturing the host cell of claim 5 under conditions in which the nucleic acid molecule is expressed.

13. A method for detecting the presence of a polypeptide of claim 8 in a sample, comprising:

a) contacting the sample with a compound which selectively binds with a polypeptide of claim 8; and

b) determining whether the compound binds with the polypeptide in the sample.

14. The method of claim 13, wherein the compound that binds with the polypeptide is an antibody.

15. A kit comprising a compound that selectively binds with a polypeptide of claim 8 and instructions for use.

16. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample, comprising the steps of:

a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes with the nucleic acid molecule; and

b) determining whether the nucleic acid probe or primer binds with a nucleic acid molecule in the sample.

17. The method of claim 16, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

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18. A kit comprising a compound that selectively hybridizes with a nucleic acid molecule of claim 1 and instructions for use.

19. A method for identifying a compound which binds with a polypeptide of claim 8 comprising the steps of:

a) contacting a polypeptide, or a cell expressing a polypeptide of claim 8 with a test compound; and

b) determining whether the polypeptide binds with the test compound.

20. The method of claim 19, wherein the binding of the test compound with the polypeptide is detected by a method selected from the group consisting of:

a) detection of binding by direct detecting of test compound/polypeptide binding;

b) detection of binding using a competition binding assay; and

c) detection of binding using an assay for 13245-mediated signal transduction.

21. A method for modulating the activity of a polypeptide of claim 8 comprising contacting a polypeptide or a cell expressing a polypeptide of claim 8 with a compound which binds with the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

22. A method for identifying a compound which modulates the activity of a polypeptide of claim 8, comprising:

a) contacting a polypeptide of claim 8 with a test compound; and

b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

23. A method of modulating the ability of a cell to catalyze interconversion of the phosphorylated and de-phosphorylated forms a GTPase protein, the method comprising

modulating 13245 protein activity in the cell, whereby the ability of the cell to phosphorylate the GTPase is modulated.

24. The method of claim 23, wherein 13245 protein activity is modulated by modulating expression of the 13245 gene in the cell.

25. The method of claim 24, wherein expression of the 13245 gene is inhibited by administering to the cell an antisense oligonucleotide which hybridizes under stringent conditions with a transcript of the 13245 gene.

26. The method of claim 25, wherein the antisense oligonucleotide comprises at least 15 nucleotide residues.

27. The method of claim 25, wherein the transcript is an mRNA.

28. The method of claim 24, wherein expression of the 13245 gene is inhibited by administering to the cell an antisense oligonucleotide which hybridizes under stringent conditions with a polynucleotide having the nucleotide sequence SEQ ID NO: 1.

29. The method of claim 24, wherein expression of the 13245 gene is inhibited by administering to the cell an antisense oligonucleotide which hybridizes under stringent conditions with a polynucleotide having the nucleotide sequence SEQ ID NO: 3.

30. The method of claim 23, wherein 13245 protein activity is modulated without significantly affecting 13245 gene expression in the cell.

31. The method of claim 23, wherein 13245 protein activity is inhibited by administering to the cell an agent which inhibits protein kinase activity.

32. The method of claim 31, wherein the agent is an antibody which specifically binds with 13245 protein.

33. The method of claim 31, wherein the activity is ability to de-phosphorylate a phosphorylated serine residue, a phosphorylated tyrosine residue, and a phosphorylated threonine residue of the substrate protein.

34. The method of claim 31, wherein the activity is ability to modulate the phosphorylation state of a Rho GTPase.

35. The method of claim 31, wherein the activity is ability to modulate a cytological effect of HIV-1 infection in a host cell.

36. The method of claim 31, wherein the activity is ability to modulate transcription of a gene in an HIV-1-infected cell.

37. The method of claim 36, wherein the cell is a peripheral blood cell.

38. The method of claim 23, wherein the cell is in the body of a human.

39. A method for assessing whether a test compound is useful for modulating at least one phenomenon selected from the group consisting of (1) interconversion of the phosphorylated and de-phosphorylated forms of a serine, threonine, or tyrosine residue of a GTPase protein; (2) cell contractility; (3) cell growth; (4) cell conductivity; (5) entry of a cell into the cell cycle; (6) progression of a cell through the cell cycle; (7) mitogenesis; (8) cell metabolism; (9) gene transcription; (11) cytokinesis; (12) cell shape; (13) cell movement; (14) integration of a viral genome into a host cell genome; (15) maintenance of a viral genome within a host cell genome; (16) a cytological change in a virus-infected host cell; (17) virus production in a virus-infected host cell; (18) interaction of a virion with a membrane of a virus-

infected host cell; and (19) encapsulation of a virion within a portion of a membrane of a virus-infected host cell, the method comprising:

a) adding the test compound to a first composition comprising a polypeptide that has an amino acid sequence at least 90% identical to SEQ ID NO: 2 and that exhibits a 13245 activity; and

b) comparing the 13245 activity in the first composition and in a second composition that is substantially identical to the first composition except that it does not comprise the test compound,

whereby a difference in the 13245 activity in the first and second compositions is an indication that the test compound is useful for modulating the phenomenon.

40. The method of claim 39, wherein the activity is GTPase kinase activity.

41. The method of claim 39, wherein the protein has the amino acid sequence SEQ ID NO: 2.

42. The method of claim 39, wherein the composition comprises a cell comprising a nucleic acid encoding the protein.

43. The method of claim 42, wherein the nucleic acid is the genome of the cell.

44. The method of claim 42, wherein the nucleic acid comprises the 13245 gene.

45. A method for assessing whether a test compound is useful for modulating at least one phenomenon selected from the group consisting of (1) interconversion of the phosphorylated and de-phosphorylated forms of a serine, threonine, or tyrosine residue of a

GTPase protein; (2) cell contractility; (3) cell growth; (4) cell conductivity; (5) entry of a cell into the cell cycle; (6) progression of a cell through the cell cycle; (7) mitogenesis; (8) cell metabolism; (9) gene transcription; (11) cytokinesis; (12) cell shape; (13) cell movement; (14) integration of a viral genome into a host cell genome; (15) maintenance of a viral genome within a host cell genome; (16) a cytological change in a virus-infected host cell; (17) virus production in a virus-infected host cell; (18) interaction of a virion with a membrane of a virus-infected host cell; and (19) encapsulation of a virion within a portion of a membrane of a virus-infected host cell, the method comprising:

a) adding the test compound to a first composition comprising a cell which comprises a nucleic acid that encodes a polypeptide that has an amino acid sequence at least 90% identical to SEQ ID NO: 2 and that exhibits a 13245 activity; and

b) comparing 13245 activity in the first composition and in a second composition that is substantially identical to the first composition except that it does not comprise the test compound,

whereby a difference in the 13245 activity in the first and second compositions is an indication that the test compound is useful for modulating the phenomenon.

46. A method of making a pharmaceutical composition for modulating at least one phenomenon selected from the group consisting of (1) interconversion of the phosphorylated and de-phosphorylated forms of a serine, threonine, or tyrosine residue of a GTPase protein; (2) cell contractility; (3) cell growth; (4) cell conductivity; (5) entry of a cell into the cell cycle; (6) progression of a cell through the cell cycle; (7) mitogenesis; (8) cell metabolism; (9) gene transcription; (11) cytokinesis; (12) cell shape; (13) cell movement; (14) integration of a viral genome into a host cell genome; (15) maintenance of a viral genome within a host cell genome; (16) a cytological change in a virus-infected host cell; (17) virus production in a virus-infected host cell; (18) interaction of a virion with a membrane of a virus-

infected host cell; and (19) encapsulation of a virion within a portion of a membrane of a virus-infected host cell, the method comprising:

a) selecting a test compound useful for modulating the phenomenon according to the method of claim 39; and

b) combining the test compound with a pharmaceutically acceptable carrier in order to make the pharmaceutical composition.

47. A method of modulating, in a human, at least one phenomenon selected from the group consisting of (1) interconversion of the phosphorylated and de-phosphorylated forms of a serine, threonine, or tyrosine residue of a GTPase protein; (2) cell contractility; (3) cell growth; (4) cell conductivity; (5) entry of a cell into the cell cycle; (6) progression of a cell through the cell cycle; (7) mitogenesis; (8) cell metabolism; (9) gene transcription; (11) cytokinesis; (12) cell shape; (13) cell movement; (14) integration of a viral genome into a host cell genome; (15) maintenance of a viral genome within a host cell genome; (16) a cytological change in a virus-infected host cell; (17) virus production in a virus-infected host cell; (18) interaction of a virion with a membrane of a virus-infected host cell; and (19) encapsulation of a virion within a portion of a membrane of a virus-infected host cell, the method comprising administering the pharmaceutical composition of claim 46 to the human in an amount effective to modulate the phenomenon.

48. A method for identifying a compound useful for modulating at least one phenomenon selected from the group consisting of (1) interconversion of the phosphorylated and de-phosphorylated forms of a serine, threonine, or tyrosine residue of a GTPase protein; (2) cell contractility; (3) cell growth; (4) cell conductivity; (5) entry of a cell into the cell cycle; (6) progression of a cell through the cell cycle; (7) mitogenesis; (8) cell metabolism; (9) gene transcription; (11) cytokinesis; (12) cell shape; (13) cell movement; (14) integration of a viral genome into a host cell genome; (15) maintenance of a viral genome within a host cell genome; (16) a cytological change in a virus-infected host cell; (17) virus production in a virus-infected

host cell; (18) interaction of a virion with a membrane of a virus-infected host cell; and (19) encapsulation of a virion within a portion of a membrane of a virus-infected host cell, the method comprising:

a) contacting the test compound and a polypeptide selected from the group consisting of

i) a polypeptide which is encoded by a nucleic acid molecule comprising a portion having a nucleotide sequence which is at least 90% identical to one of SEQ ID NOs: 1 and 3; and

ii) a fragment of a polypeptide having either an amino acid sequence comprising SEQ ID NO: 2, wherein the fragment comprises at least 25 contiguous amino acid residues of SEQ ID NO: 2

or a cell that expresses the polypeptide; and

b) determining whether the polypeptide binds with the test compound,

whereby binding of the polypeptide and the test compound is an indication that the test compound is useful for modulating the phenomenon.

49. The method of claim 48, wherein the polypeptide exhibits an epitope in common with a polypeptide having the amino acid sequence SEQ ID NO: 2.